


```

/sex="female"
/lab_host="DH10B"
/proc="Jordan; Kidney/Brain; Vector: pBAC3.6; Site_1:
EcoRI; Site_2: EcoRI; Female c7781/6j mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI-Methylase. Slice
selected DNA was cloned into the pBAC3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)."
BASE COUNT      47 a      46 c      56 g      45 t
ORIGIN
alignment_scores:
  Quality:      44.00      Length:      34
  Ratio:      1.000      Gaps:      0
  Percent Similarity: 100.000      Percent Identity: 100.000
alignment_block:
  US-09-126-945b-2_copy_2_335 x AZ090824/rev
Align seq 1/1 to reverse of: AZ090824 from: 1 to: 174
400 AsnTfYAspIysIeGSeTArGSeGIIleArGcItTtYtTylsIysGlyI 416
|||||
171 AACATATGATTAACATTAACGCGCCGACATTTACAAAGCGGCAT 122
416 cIleArGlySeTArGSeGIIleArGcItTtYtTylsIysGlyI 433
|||||
121 CATTCGTAAACCGCAATCTTCACGCGCTTGTGTACCAATTGTGATC 72
443 to 444
11
71 CA 70
seq_name: qb_gst24:A1745526
seq_documentation_block:
  LOCUS      A1745526      721 bp      mRNA
  DEFINITION      wc14410.x1 NCI-CCAP_Pt28 Homo sapiens cDNA clone IMAGE:217050 3'
  similar to: SM-EFSA_DBHOME P29775 DNA-BINDING PROTEIN D-ETS-4 ; mRNA
  sequence.
  ACCESSION      A1745526
  VERSION        A1745526.1      GI:5111814
  KEYWORDS      EST.
  SOURCE        human.
  ORGANISM      Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE      1 (bases 1 to 721)
  AUTHORS      NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicqap.
  TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
  JOURNAL      Unpublished (1997)
  COMMENT      Contact: Robert Strausberg, Ph.D.
  Email: rgraphs@mail.nih.gov
  Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
  Hammer-Buck, M.D., Ph.D.
  cDNA Library Preparation: M. Bento Soares, Ph.D.
  cDNA Library Arrayed by: Greg Lennon, Ph.D.
  DNA Sequencing by: Washington University Genome Sequencing Center
  Clone distribution: NCI-CCAP clone distribution information can be
  found through the I.M.A.G.E. Consortium/ILMI, at:
  www.bio.lit.gov/hbrp/imag/imag.html
  Insert length: 826      Std Error: 0.00
  Seq primer: -400p from Gibco
  High quality sequence stop: 448.
  Location/Qualifiers
  1..721
  /organism="Homo sapiens"
  /db_xref="taxon:9606"
  /clone_lib="NCI-CCAP_Pt28"
  /sex="female"
  /dev_stage="adult"

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/sex="male"
/dev_stage="adult"
/lab_host="DH10B"
/proc="Jordan; prostate; Vector: pTZ19-pac (Pharmacia)
with a modified polylinker. Plasmid DNA from the
normalized library NCI-CCAP_Pt28 was prepared, and ss
circles were made in vitro. Following DNA purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clonethus
985608-986759, 1101192-1101959, and 1217928-1220615)."
BASE COUNT      122 a      197 c      241 g      156 t
ORIGIN
alignment_scores:
  Quality:      33.00      Length:      33
  Ratio:      1.000      Gaps:      0
  Percent Similarity: 100.000      Percent Identity: 100.000
alignment_block:
  US-09-126-945b-2_copy_2_335 x A1745526/rev
Align seq 1/1 to reverse of: A1745526 from: 1 to: 721
279 LysIleGluAspSerAlaGlnValAlaArgIleuTrpGlyIleArgLysAs 295
|||||
642 AAATTTGAGGACATGAGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCG 593
295 nArGPrOAlaMeTAsnTfYAspIysIeGSeTArGSeGIIleArGcItTtY 311
|||||
592 CCGTCCCGCATGACATGACATGACATGACATGACATGACATGACATGACAT 544
seq_name: qb_est87:BF446190
seq_documentation_block:
  LOCUS      BF446190      625 bp      mRNA
  DEFINITION      TP3108.x1 NCI-CCAP_Pt28 Homo sapiens cDNA clone IMAGE:3647751 3'
  similar to: TP-095238 095238 EST TRANSCRIPTION FACTOR POFB. ; mRNA
  sequence.
  ACCESSION      BF446190
  VERSION        BF446190.1      GI:11511328
  KEYWORDS      EST.
  SOURCE        human.
  ORGANISM      Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE      1 (bases 1 to 625)
  AUTHORS      NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicqap.
  TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
  JOURNAL      Unpublished (1997)
  COMMENT      Contact: Robert Strausberg, Ph.D.
  Email: rgraphs@mail.nih.gov
  Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
  Hammer-Buck, M.D., Ph.D.
  cDNA Library Preparation: M. Bento Soares, Ph.D.
  cDNA Library Arrayed by: Greg Lennon, Ph.D.
  DNA Sequencing by: Washington University Genome Sequencing Center
  Clone distribution: NCI-CCAP clone distribution information can be
  found through the I.M.A.G.E. Consortium/ILMI, send email to:
  info@image.lit.gov
  Seq primer: -400p from Gibco
  High quality sequence stop: 460.
  Location/Qualifiers
  1..625
  /organism="Homo sapiens"
  /db_xref="taxon:9606"
  /clone_lib="NCI-CCAP_Pt28"
  /sex="male"
  /dev_stage="adult"

```


/lab_host-"DH10B"
 /note-"Organ: prostate; Vector: pT73D-Pac (Pharmacia)
 with a modified polylinker; Plasmid DNA from the
 normalized library NCI_CGAP_Fr22 was prepared, and ss
 clones were made in vitro. Following HAP purification,
 this DNA was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from a pool
 of 5,000 clones made from the same library (clones IDs
 985608-986759, 1101192-1101959, and 1217928-1228615).
 Subtraction by Benito Soares and M. Patricia Ronaldo."

BASE COUNT 113 a 174 c 202 g 135 t 1 others

ALIGNMENT_SCORES:

Quality: 32.00 Length: 32
 Ratio: 1.000 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

ALIGNMENT_BLOCK:

US-09-126-945B-2_COPY_2_335 x BF446196/rev ..

Align seg 1/1 to reverse of: BF446190 from: 1 to: 625

303 LysleuserArgserLeArgGlnTyrTyrLysGlylleArgArgly 319
 ||||||||||||||||||||||||||||||||||||||||||||
 581 AAGCTGAGCCGCTCCATCCGCCATATTACAGACAGCGCATCATCCGAA 532
 319 sProAspLleSerGlnArgLeuValTyrGlnPheValHisProIle 334
 ||||||||||||||||||||||||||||||||||||||||||||
 531 GTCATATATCTCCAGACGCTCTGCTACGTGCTGTCACACCCCAT 486

seq_name: qb_cst189;BF579116

seq_documentation_block:

LOCUS BF579116 2064 bp mRNA EST 12-DEC-2000
 DEFINITION 602046650P1 NCI_CGAP_0624 Mus musculus cDNA clone IMAGE:4215901 5',
 mRNA sequence.

ACCESSION BF579116
 VERSION BF579116.1 GI:11652828

KEYWORDS:

EST.

SOURCE:

house mouse.

ORGANISM:

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;

1 (bases 1 to 2064)

NIH-MDC http://mgi.mgi.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgarbs@mail.nih.gov

Tissue procurement: Jeffrey E. Green, M.D.

cDNA library preparation: Life Technologies, Inc.

cDNA library Arrayed by: The I M A G E Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

http://image.llnl.gov

plate: LLAM9792 row: d column: 14

High quality sequence stop: 645.

Location/Qualifiers

1..2064

/organism="Mus musculus"

/strain="FVB/N"

/db_xref="taxon:10090"

/clone="IMAGE:4215901"

/lab_host="NCI_CGAP_Co24"

/note="Organ: prostate; Vector: pT73D-Pac (Pharmacia)
 with a modified polylinker; Plasmid DNA from the
 normalized library NCI_CGAP_Fr22 was prepared, and ss
 clones were made in vitro. Following HAP purification,
 this DNA was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from a pool
 of 5,000 clones made from the same library (clones IDs
 985608-986759, 1101192-1101959, and 1217928-1228615).
 Subtraction by Benito Soares and M. Patricia Ronaldo."

BASE COUNT 624 a 621 c 620 g 199 t

ORIGIN

ALIGNMENT_SCORES:
 Quality: 32.00 Length: 32
 Ratio: 1.000 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

ALIGNMENT_BLOCK:

US-09-126-945B-2_COPY_2_335 x BF579116 ..

Align seg 1/1 to: BF579116 from: 1 to: 2064

115 GluHisSerLeuGlnValGlnSerMetValValGlyGluValLeu 131
 ||||||||||||||||||||||||||||||||||||||||||||
 302 GAGGACTGGCTAGAGAGCTGCAATGATGTTGTGGGCGAGGTCCTGAA 351
 131 SASPIleGluThrAlaGlySerLeuLeuValSerIleThrAlaAspPro 146
 ||||||||||||||||||||||||||||||||||||||||||||
 352 AGATATTAAGACGAGCTCAAGATTAAGATTAAGATTAAGATTAAGAT 397

